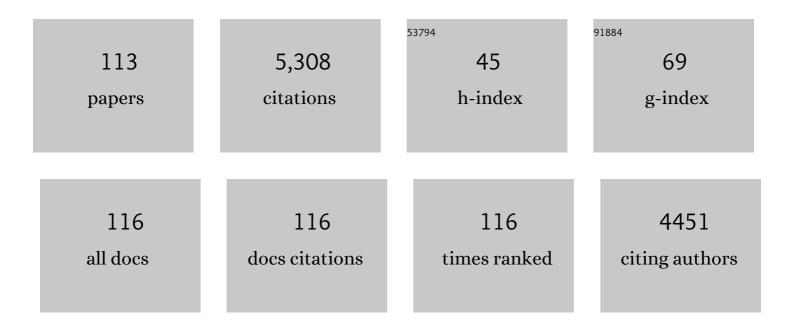
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Novel Thienopyrimidine Inhibitors of <i>Leishmania N</i> -Myristoyltransferase with On-Target Activity in Intracellular Amastigotes. Journal of Medicinal Chemistry, 2020, 63, 7740-7765.	6.4	15
2	Fragment-derived inhibitors of human N-myristoyltransferase block capsid assembly and replication of the common cold virus. Nature Chemistry, 2018, 10, 599-606.	13.6	96
3	A tri-functional vanadium(<scp>iv</scp>) complex to detect cysteine oxidation. Dalton Transactions, 2017, 46, 6994-7004.	3.3	6
4	Structure-guided optimization of quinoline inhibitors of Plasmodium N-myristoyltransferase. MedChemComm, 2017, 8, 191-197.	3.4	14
5	Vanadyl complexes with dansyl-labelled di-picolinic acid ligands: synthesis, phosphatase inhibition activity and cellular uptake studies. Dalton Transactions, 2016, 45, 7104-7113.	3.3	4
6	Synchronized Optical and Electronic Detection of Biomolecules Using a Low Noise Nanopore Platform. ACS Nano, 2015, 9, 1740-1748.	14.6	62
7	Discovery of pyridyl-based inhibitors of Plasmodium falciparum N-myristoyltransferase. MedChemComm, 2015, 6, 1767-1772.	3.4	13
8	Discovery of high affinity inhibitors of Leishmania donovani N-myristoyltransferase. MedChemComm, 2015, 6, 1761-1766.	3.4	30
9	Using a Non-Image-Based Medium-Throughput Assay for Screening Compounds Targeting N-myristoylation in Intracellular Leishmania Amastigotes. PLoS Neglected Tropical Diseases, 2014, 8, e3363.	3.0	16
10	Design and synthesis of irreversible inhibitors of foot-and-mouth disease virus 3C protease. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 490-494.	2.2	7
11	Design and Synthesis of High Affinity Inhibitors of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax N</i> -Myristoyltransferases Directed by Ligand Efficiency Dependent Lipophilicity (LELP). Journal of Medicinal Chemistry, 2014, 57, 2773-2788.	6.4	63
12	Validation of N-myristoyltransferase as an antimalarial drug target using an integrated chemical biology approach. Nature Chemistry, 2014, 6, 112-121.	13.6	196
13	Diverse modes of binding in structures of <i>Leishmania majorN</i> myristoyltransferase with selective inhibitors. IUCrJ, 2014, 1, 250-260.	2.2	38
14	Structure-Based Design of Potent and Selective <i>Leishmania N</i> -Myristoyltransferase Inhibitors. Journal of Medicinal Chemistry, 2014, 57, 8664-8670.	6.4	56
15	Peptidomimetic inhibitors of <i>N</i> -myristoyltransferase from human malaria and leishmaniasis parasites. Organic and Biomolecular Chemistry, 2014, 12, 8132-8137.	2.8	30
16	Potent and specific inhibition of the biological activity of the type-II transmembrane serine protease matriptase by the cyclic microprotein MCoTI-II. Thrombosis and Haemostasis, 2014, 112, 402-411.	3.4	27
17	Enantioselective synthesis of (+)-aspercyclide A. Tetrahedron Letters, 2013, 54, 4970-4972.	1.4	10
18	Development of small molecules to target the IgE:FcεRI protein–protein interaction in allergies. Future Medicinal Chemistry, 2013, 5, 1423-1435.	2.3	12

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19	Discovery of Novel and Ligand-Efficient Inhibitors of Plasmodium falciparum and Plasmodium vivax <i>N</i> -Myristoyltransferase. Journal of Medicinal Chemistry, 2013, 56, 371-375.	6.4	58
20	Selective Inhibitors of Protozoan Protein N-myristoyltransferases as Starting Points for Tropical Disease Medicinal Chemistry Programs. PLoS Neglected Tropical Diseases, 2012, 6, e1625.	3.0	79
21	Droplet dispensing in digital microfluidic devices: Assessment of long-term reproducibility. Biomicrofluidics, 2012, 6, 22003-2200310.	2.4	19
22	Discovery of Plasmodium vivax <i>N</i> -Myristoyltransferase Inhibitors: Screening, Synthesis, and Structural Characterization of their Binding Mode. Journal of Medicinal Chemistry, 2012, 55, 3578-3582.	6.4	65
23	Design and Synthesis of Inhibitors of <i>Plasmodium falciparumN</i> -Myristoyltransferase, A Promising Target for Antimalarial Drug Discovery. Journal of Medicinal Chemistry, 2012, 55, 8879-8890.	6.4	56
24	Synthesis and Incorporation into Cyclic Peptides of Tolan Amino Acids and Their Hydrogenated Congeners: Construction of an Array of A–B-loop Mimetics of the Cε3 Domain of Human IgE. Journal of Organic Chemistry, 2012, 77, 3197-3214.	3.2	21
25	Mutational Locally Enhanced Sampling (MULES) for quantitative prediction of the effects of mutations at protein–protein interfaces. Chemical Science, 2012, 3, 1503.	7.4	2
26	A fluorescence-based assay for N-myristoyltransferase activity. Analytical Biochemistry, 2012, 421, 342-344.	2.4	69
27	Synthesis of the C19 methyl ether of aspercyclide A via germyl-Stille macrocyclisation and ELISA evaluation of both enantiomers following optical resolution. Organic and Biomolecular Chemistry, 2011, 9, 6814.	2.8	10
28	Comparing experimental and computational alanine scanning techniques for probing a prototypical protein–protein interaction. Protein Engineering, Design and Selection, 2011, 24, 197-207.	2.1	73
29	A Two-step Mechanism for the Folding of Actin by the Yeast Cytosolic Chaperonin. Journal of Biological Chemistry, 2011, 286, 178-184.	3.4	26
30	Organic Solvent Nanofiltration: A New Paradigm in Peptide Synthesis. Organic Process Research and Development, 2010, 14, 1313-1325.	2.7	45
31	Insights into Cleavage Specificity from the Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease Complexed with a Peptide Substrate. Journal of Molecular Biology, 2010, 395, 375-389.	4.2	63
32	N-Myristoyltransferase from Leishmania donovani: Structural and Functional Characterisation of a Potential Drug Target for Visceral Leishmaniasis. Journal of Molecular Biology, 2010, 396, 985-999.	4.2	98
33	Membrane enhanced peptide synthesis. Chemical Communications, 2010, 46, 2808.	4.1	42
34	Total synthesis of (±)-aspercyclide A and its C19 methyl ether. Chemical Communications, 2010, 46, 1824-1826.	4.1	31
35	Analysis of Protein–Protein Interactions by Using Dropletâ€Based Microfluidics. ChemBioChem, 2009, 10, 1605-1611.	2.6	60
36	Potent Inhibitors of β-Tryptase and Human Leukocyte Elastase Based on the MCoTI-II Scaffold. Journal of Medicinal Chemistry, 2009, 52, 6197-6200.	6.4	126

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37	<i>N</i> â€Myristoyltransferase: a Prospective Drug Target for Protozoan Parasites. ChemMedChem, 2008, 3, 402-408.	3.2	60
38	N-Myristoyl transferase-mediated protein labelling in vivo. Organic and Biomolecular Chemistry, 2008, 6, 2308.	2.8	128
39	Specific N-terminal protein labelling: use of FMDV 3Cpro protease and native chemical ligation. Chemical Communications, 2008, , 3369.	4.1	27
40	Site-specific N-terminal labelling of proteinsin vitro and in vivo using N-myristoyl transferase and bioorthogonal ligation chemistry. Chemical Communications, 2008, , 480-482.	4.1	78
41	Chemical and biomimetic total syntheses of natural and engineered MCoTI cyclotides. Organic and Biomolecular Chemistry, 2008, 6, 1462.	2.8	148
42	Molecules incorporating a benzothiazole core scaffold inhibit the N-myristoyltransferase of <i>Plasmodium falciparum</i> . Biochemical Journal, 2007, 408, 173-180.	3.7	61
43	Structural and Mutagenic Analysis of Foot-and-Mouth Disease Virus 3C Protease Reveals the Role of the β-Ribbon in Proteolysis. Journal of Virology, 2007, 81, 115-124.	3.4	81
44	Foot-and-mouth disease virus 3C protease: Recent structural and functional insights into an antiviral target. International Journal of Biochemistry and Cell Biology, 2007, 39, 1-6.	2.8	58
45	Immobilized Protease-Assisted Synthesis of Engineered Cysteine-Knot Microproteins. ChemBioChem, 2007, 8, 1107-1109.	2.6	46
46	Resisting degradation by human elastase: Commonality of design features shared by â€~canonical' plant and bacterial macrocyclic protease inhibitor scaffolds. Bioorganic and Medicinal Chemistry, 2007, 15, 4618-4628.	3.0	5
47	A continuous assay for foot-and-mouth disease virus 3C protease activity. Analytical Biochemistry, 2007, 368, 130-137.	2.4	16
48	Total synthesis of the macrocyclic cysteine knot microprotein MCoTI-II. Chemical Communications, 2006, , 2848.	4.1	55
49	Peptide-based inhibitors ofN-myristoyl transferase generated from a lipid/combinatorial peptide chimera library. Signal Transduction, 2006, 6, 160-166.	0.4	5
50	Characterization and selective inhibition of myristoyl-CoA:protein N-myristoyltransferase from Trypanosoma brucei and Leishmania major. Biochemical Journal, 2006, 396, 277-285.	3.7	57
51	Reagent-Controlled Stereoselective Synthesis of Lignan-Related Tetrahydrofurans ChemInform, 2005, 36, no.	0.0	0
52	A Novel, Stereoselective and Convergent Synthesis of Aryltetralins ChemInform, 2005, 36, no.	0.0	0
53	Analysis of calibration methodologies for solvent effects in drug discovery studies using evanescent wave biosensors. Biosensors and Bioelectronics, 2005, 21, 128-134.	10.1	6
54	Solution Structure of a Novel C2-Symmetrical Bifunctional Bicyclic Inhibitor Based on SFTI-1. Journal of Biomolecular NMR, 2005, 33, 57-62.	2.8	12

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55	Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease. Journal of Biological Chemistry, 2005, 280, 11520-11527.	3.4	126
56	Design, synthesis and analysis of novel bicyclic and bifunctional protease inhibitors. Protein Engineering, Design and Selection, 2004, 17, 681-687.	2.1	33
57	Inhibition of human β-tryptase by Bowman–Birk inhibitor derived peptides: creation of a new tri-functional inhibitor. Bioorganic and Medicinal Chemistry, 2004, 12, 6045-6052.	3.0	20
58	Synthesis and bio-assay of RCM-derived Bowman–Birk inhibitor analogues. Organic and Biomolecular Chemistry, 2004, 2, 281-283.	2.8	29
59	Reagent-Controlled Stereoselective Synthesis of Lignan-Related Tetrahydrofurans. Journal of Organic Chemistry, 2004, 69, 6874-6882.	3.2	76
60	A novel, stereoselective and convergent synthesis of aryltetralins. Chemical Communications, 2004, , 2292.	4.1	11
61	The conserved P1′ Ser of Bowman–Birk-type proteinase inhibitors is not essential for the integrity of the reactive site loop. Biochemical and Biophysical Research Communications, 2003, 308, 300-305.	2.1	14
62	The Structural Basis of a Conserved P2 Threonine in Canonical Serine Proteinase Inhibitors. Journal of Biomolecular Structure and Dynamics, 2003, 20, 645-655.	3.5	10
63	The1H-NMR Solution Structure of the Antitryptic Core Peptide of Bowman-Birk Inhibitor Proteins: A Minimal †Canonical Loop'. Journal of Biomolecular Structure and Dynamics, 2002, 20, 59-70.	3.5	25
64	A Conserved cis Peptide Bond Is Necessary for the Activity of Bowman-Birk Inhibitor Protein. Biochemistry, 2002, 41, 10608-10615.	2.5	54
65	Peptide mimics of the Bowman-Birk inhibitor reactive site loop. Biopolymers, 2002, 66, 79-92.	2.4	86
66	Inhibition of human βâ€ŧryptase by Bowman–Birk inhibitor derived peptides. Chemical Biology and Drug Design, 2002, 59, 90-93.	1.1	7
67	The Bowman-Birk inhibitor reactive site loop sequence represents an independent structural β-hairpin motif. Journal of Molecular Biology, 2001, 306, 799-807.	4.2	45
68	Introduction of the new dipeptide isostere 7-endo-BtA as reverse turn inducer in a Bowman-Birk proteinase inhibitor. Bioorganic and Medicinal Chemistry, 2001, 9, 1625-1632.	3.0	18
69	Synthetic Peptide Mimics of the Bowman-Birk Inhibitor Protein. Current Medicinal Chemistry, 2001, 8, 909-917.	2.4	50
70	Synthesis and Activity of a Small Cyclic Protease Inhibitor from Sunflower Seeds, SFTI-1. , 2001, , 547-548.		1
71	Screening and Synthesis of a Positional Scanning Library Based on the Bowman-Birk Reactive Site Loop. , 2001, , 196-197.		0
72	Identification of chymotrypsin inhibitors from a second-generation template assisted combinatorial peptide library. Journal of Peptide Science, 2000, 6, 446-452.	1.4	19

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73	Identification of chymotrypsin inhibitors from a second-generation template assisted combinatorial peptide library. Journal of Peptide Science, 2000, 6, 446.	1.4	Ο
74	Analysis of molecular recognition using optical biosensors. Current Opinion in Chemical Biology, 1999, 3, 544-547.	6.1	62
75	Selection of human elastase inhibitors from a conformationally constrained combinatorial peptide library. FEBS Journal, 1999, 266, 403-412.	0.2	42
76	The role of the P2′ position of Bowman-Birk proteinase inhibitor in the inhibition of trypsin. BBA - Proteins and Proteomics, 1999, 1431, 232-237.	2.1	38
77	A study of the specificity of barley chymotrypsin inhibitor 2 by cysteine engineering of the P1 residue. BBA - Proteins and Proteomics, 1998, 1384, 325-334.	2.1	3
78	Second-Order Kinetic Analysis of IAsys Biosensor Data: Its Use and Applicability. Analytical Biochemistry, 1998, 263, 1-12.	2.4	45
79	Effect of Osmolytes on the Exchange Rates of Backbone Amide Protons in Proteins. Biochemistry, 1998, 37, 2969-2978.	2.5	66
80	The role of threonine in the P 2 position of bowman-birk proteinase inhibitors: studies on P 2 variation in cyclic peptides encompassing the reactive site loop 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 282, 447-457.	4.2	44
81	Determination of Association Rate Constants by an Optical Biosensor Using Initial Rate Analysis. Analytical Biochemistry, 1997, 246, 1-6.	2.4	74
82	Stability of protease inhibitors based on the Bowmanâ€Birk reactive site loop to hydrolysis by proteases. Chemical Biology and Drug Design, 1997, 49, 467-475.	1.1	25
83	Analysis of kinetic data of antibody-antigen interaction from an optical biosensor by exponential curve fitting. Journal of Biotechnology, 1996, 48, 117-127.	3.8	22
84	Selection of Chymotrypsin Inhibitors from a Conformationally-constrained Combinatorial Peptide Library. Journal of Molecular Biology, 1996, 259, 819-827.	4.2	71
85	Kinetics of Protein-Protein Interactions at the Surface of an Optical Biosensor. Analytical Biochemistry, 1995, 231, 210-217.	2.4	187
86	Synthesis of a mixture of cyclic peptides based on the Bowmanâ€Birk reactive site loop to screen for serine protease inhibitors. International Journal of Peptide and Protein Research, 1995, 46, 79-87.	0.1	39
87	Expression and kinetic characterization of barley chymotrypsin inhibitors 1a and 1b. Biochimica Et Biophysica Acta - Molecular Cell Research, 1994, 1222, 179-186.	4.1	8
88	Carbon-13 NMR study of the effects of mutation on the tryptophan dynamics in chymotrypsin inhibitor 2: correlations with structure and stability. Biochemistry, 1993, 32, 657-662.	2.5	22
89	Carbon-13 NMR study of the effects of mutation on the tryptophan dynamics in chymotrypsin inhibitor 2: correlations with structure and stability. [Erratum to document cited in CA118(5):34967r]. Biochemistry, 1993, 32, 4474-4474.	2.5	0
90	Imaging of proteins by scanning tunnelling microscopy. Ultramicroscopy, 1992, 42-44, 1200-1203.	1.9	8

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91	Carbon-13 nuclear magnetic resonance relaxation study of chymotrypsin inhibitor 2 (CI-2). Magnetic Resonance in Chemistry, 1992, 30, 1255-1260.	1.9	3
92	Diversification of the IgG molecule by oligosaccharides. Molecular Immunology, 1991, 28, 1369-1378.	2.2	67
93	Design of a small peptide-based proteinase inhibitor by modeling the active-site region of barley chymotrypsin inhibitor 2. Biochemistry, 1991, 30, 10717-10721.	2.5	22
94	Structure of immunoglobulin G by scanning tunnelling microscopy. Journal of Molecular Biology, 1991, 221, 361-365.	4.2	43
95	Use of nonlinear regression to analyze enzyme kinetic data: Application to situations of substrate contamination and background subtraction. Analytical Biochemistry, 1990, 184, 274-278.	2.4	31
96	Role of arginine 67 in the stabilization of chymotrypsin inhibitor 2: examination of amide proton exchange rates and denaturation thermodynamics of an engineered protein. Biochemistry, 1990, 29, 6264-6269.	2.5	50
97	Metal ion dependence of phosphorothioate ATP analogs in the Bacillus stearothermophilus tyrosyl-tRNA synthetase. Biochemistry, 1990, 29, 1643-1648.	2.5	10
98	Bovine dopamine .betahydroxylase, primary structure determined by cDNA cloning and amino acid sequencing. Biochemistry, 1990, 29, 6466-6474.	2.5	22
99	Using linear and non-linear regression to fit biochemical data. Trends in Biochemical Sciences, 1990, 15, 455-458.	7.5	192
100	Designer catalytic antibodies. Nature, 1989, 338, 206-207.	27.8	3
101	Investigation of transition-state stabilization by residues histidine-45 and threonine-40 in the tyrosyl-tRNA synthetase. Biochemistry, 1987, 26, 8524-8528.	2.5	42
102	Structure-activity relationships in engineered proteins: analysis of use of binding energy by linear free energy relationships. Biochemistry, 1987, 26, 6030-6038.	2.5	155
103	Protein engineering. Protein Engineering, Design and Selection, 1986, 1, 7-16.	2.1	99
104	Binding energy and catalysis: a lesson from protein engineering of the tyrosyl-tRNA synthetase. Trends in Biochemical Sciences, 1986, 11, 321-325.	7.5	84
105	Structure and activity of the tyrosy1-tRNA synthetase: the hydrogen bond in catalysis and specificity. Philosophical Transactions of the Royal Society A, 1986, 317, 305-320.	1.1	20
106	Quantitative analysis of structure–activity relationships in engineered proteins by linear free-energy relationships. Nature, 1986, 322, 284-286.	27.8	111
107	Transition-state stabilization in the mechanism of tyrosyl-tRNA synthetase revealed by protein engineering Proceedings of the National Academy of Sciences of the United States of America, 1985, 82, 7840-7844.	7.1	180
108	Effector functions of a monoclonal aglycosylated mouse IgG2a: Binding and activation of complement component C1 and interaction with human monocyte Fc receptor. Molecular Immunology, 1985, 22, 407-415.	2.2	199

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109	Binding of complement subcomponent Clq to mouse IgGl, IgG2a AND IgG2b: A novel Clq binding assay. Molecular Immunology, 1984, 21, 321-327.	2.2	47
110	The effect of aglycosylation on the binding of mouse IgG to staphylococcal protein A. FEBS Letters, 1983, 164, 227-230.	2.8	37
111	Role of tyrosines in the combining site of the dinitrophenyl-binding IgA myeloma M315: specific nitration and high-resolution proton nuclear magnetic resonance studies. Biochemistry, 1982, 21, 5124-5129.	2.5	12
112	A combined proton and phosphorus-31 nuclear magnetic resonance investigation of the combining site of M603, a phosphocholine-binding myeloma protein. Biochemistry, 1982, 21, 4927-4931.	2.5	10
113	Antibody specificity: a 270-MHz hydrogen-1 nuclear magnetic resonance study of the binding of dinitrophenyl compounds to the VL dimer of protein 315. Biochemistry, 1981, 20, 2339-2345.	2.5	6